



#14

# SEQUENCE LISTING

<110> Prayaga, Suhhirdas K  
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

<400> 1

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aatggtaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
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<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2

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1 5 10 15
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20 25 30  
 Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser  
 35 40 45  
 Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His  
 50 55 60  
 Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys  
 65 70 75 80  
 Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg  
 85 90 95  
 Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn  
 100 105 110  
 Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr  
 115 120 125  
 Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn  
 130 135 140  
 Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu  
 145 150

<210> 3  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (74)..(208)  
 <223> Wherein n is a or t or c or g.

<400> 3  
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 ctgcgacctg cctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180  
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 gcaccagcag atcttcagcc tctttttaca caagggttg tctgatgctt ggaatagggc 300  
 cttcttggtg aaactccaga ctggatttca tcagcagctg gaagacctg agacctgctt 360  
 tggatatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420  
 aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480  
 ctgggaggtt gtcgtaatgg taaagggtt tttcttaagc acaaaacttc aagaaaaaga 540  
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gtgaaagctg

610

<210> 4  
<211> 199  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (24)..(68)  
<223> Wherein Xaa is any amino acid.

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20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60  
Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His  
65 70 75 80  
Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp  
85 90 95  
Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu  
100 105 110  
Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser  
115 120 125  
Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln  
130 135 140  
Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp  
145 150 155 160  
Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln  
165 170 175  
Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys

180

185

190

Val Ile Tyr Leu Ala Glu Glu

195

&lt;210&gt; 5

&lt;211&gt; 1887

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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gcagccgagc tgcggctggc agacaacttc atcgccctccg tgcgcccgcg cgacctggcc 240
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1887

&lt;210&gt; 6

&lt;211&gt; 628

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala  
35 40 45

Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu  
50 55 60

Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala  
65 70 75 80

Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg  
85 90 95

His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu  
100 105 110

His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg  
115 120 125

Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala  
130 135 140

Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp  
145 150 155 160

Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu  
165 170 175

Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu  
180 185 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg  
195 200 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu  
210 215 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser  
225 230 235 240

Ala	Leu	Val	Leu	Ala	Phe	Gly	Gly	Asn	Pro	Leu	His	Cys	Asn	Cys	Glu	245	250	255
Leu	Val	Trp	Leu	Arg	Arg	Leu	Ala	Arg	Glu	Asp	Asp	Leu	Glu	Ala	Cys	260	265	270
Ala	Ser	Pro	Pro	Ala	Leu	Gly	Gly	Arg	Tyr	Phe	Trp	Ala	Val	Gly	Glu	275	280	285
Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Val	Val	Thr	His	Arg	Ser	Pro	Pro	290	295	300
Leu	Ala	Val	Pro	Ala	Gly	Arg	Pro	Ala	Ala	Leu	Arg	Cys	Arg	Ala	Val	305	310	315
Gly	Asp	Pro	Glu	Pro	Arg	Val	Arg	Trp	Val	Ser	Pro	Gln	Gly	Arg	Leu	325	330	335
Leu	Gly	Asn	Ser	Ser	Arg	Ala	Arg	Ala	Phe	Pro	Asn	Gly	Thr	Leu	Glu	340	345	350
Leu	Leu	Val	Thr	Glu	Pro	Gly	Asp	Gly	Gly	Ile	Phe	Thr	Cys	Ile	Ala	355	360	365
Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Ala	Val	Glu	Leu	Thr	Val	Gly	370	375	380
Pro	Pro	Pro	Pro	Pro	Gln	Leu	Ala	Asn	Ser	Thr	Ser	Cys	Asp	Pro	Pro	385	390	395
Arg	Asp	Gly	Asp	Pro	Asp	Ala	Leu	Thr	Pro	Pro	Ser	Ala	Ala	Ser	Ala	405	410	415
Ser	Ala	Lys	Val	Ala	Asp	Thr	Gly	Pro	Pro	Thr	Asp	Arg	Gly	Val	Gln	420	425	430
Val	Thr	Glu	His	Gly	Ala	Thr	Ala	Ala	Leu	Val	Gln	Trp	Pro	Asp	Gln	435	440	445
Arg	Pro	Ile	Pro	Gly	Ile	Arg	Met	Tyr	Gln	Ile	Gln	Tyr	Asn	Ser	Ser	450	455	460
Ala	Asp	Asp	Ile	Leu	Val	Tyr	Arg	Met	Ile	Pro	Ala	Glu	Ser	Arg	Ser	465	470	475
Phe	Leu	Leu	Thr	Asp	Leu	Ala	Ser	Gly	Arg	Thr	Tyr	Asp	Leu	Cys	Val	485	490	495

Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro  
500 505 510

Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly  
515 520 525

Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly  
530 535 540

Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met  
545 550 555 560

Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro  
565 570 575

Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro  
580 585 590

Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala  
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His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu  
610 615 620

Pro Val Gly Pro  
625

<210> 7

<211> 802

<212> DNA

<213> Equus caballus

<400> 7

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aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660  
cagcaaact gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720  
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tcttatttct gctttagtct ag

802

<210> 8

<211> 195

<212> PRT

<213> Homo sapiens

<400> 8

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			20					25					30		

Leu	Ser	Arg	Asn	Thr	Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile	Ser
		35					40					45			

Pro	Phe	Leu	Cys	Leu	Lys	Asp	Arg	Arg	Asp	Phe	Arg	Phe	Pro	Gln	Glu
	50					55					60				

Met	Val	Lys	Gly	Ser	Gln	Leu	Gln	Lys	Ala	His	Val	Met	Ser	Val	Leu
65					70					75					80

His	Glu	Met	Leu	Gln	Gln	Ile	Phe	Ser	Leu	Phe	His	Thr	Glu	Arg	Ser
			85						90					95	

Ser	Ala	Ala	Trp	Asn	Met	Thr	Leu	Leu	Asp	Gln	Leu	His	Thr	Gly	Leu
		100						105					110		

His	Gln	Gln	Leu	Gln	His	Leu	Glu	Thr	Cys	Leu	Leu	Gln	Val	Val	Gly
	115						120					125			

Glu	Gly	Glu	Ser	Ala	Gly	Ala	Ile	Ser	Ser	Pro	Ala	Leu	Thr	Leu	Arg
	130					135					140				

Arg	Tyr	Phe	Gln	Gly	Ile	Arg	Val	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser
145					150					155					160

Asp	Cys	Ala	Trp	Glu	Val	Val	Arg	Met	Glu	Ile	Met	Lys	Ser	Leu	Phe
			165						170						175

Leu	Ser	Thr	Asn	Met	Gln	Glu	Arg	Leu	Arg	Ser	Lys	Asp	Arg	Asp	Leu
			180					185					190		

Gly	Ser	Ser
	195	



<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser  
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Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu  
20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser  
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu  
65 70 75 80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu  
100 105 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly  
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys  
130 135 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu  
180 185 190

Gly Ser Pro  
195

<210> 10

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143

Domain 71-187

<400> 10

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Ile	Phe	His	Phe	Phe	Cys	Thr	Glu	Ala	Ser	Ser	Ser	Ala	Ala	Trp	Asn
			20					25					30		

Thr	Thr	Leu	Leu	Glu	Glu	Phe	Cys	Thr	Gly	Leu	Asp	Arg	Gln	Leu	Thr
		35					40					45			

Arg	Leu	Glu	Ala	Cys	Val	Leu	Gln	Glu	Val	Glu	Glu	Gly	Glu	Ala	Pro
	50					55					60				

Leu	Thr	Asn	Glu	Asp	Ile	His	Pro	Glu	Asp	Ser	Ile	Leu	Arg	Asn	Tyr
65					70					75				80	

Phe	Gln	Arg	Leu	Ser	Leu	Tyr	Leu	Gln	Glu	Lys	Lys	Tyr	Ser	Pro	Cys
				85					90					95	

Ala	Trp	Glu	Ile	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Leu	Tyr	Tyr	Ser
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Ser	Thr	Ala	Leu	Gln
			115	

<210> 11

<211> 194

<212> PRT

<213> Felis catus

<400> 11

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Asn	Ser	Val	Cys	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Gly	Leu
			20					25					30		

Leu	Asn	Arg	Arg	Ala	Leu	Thr	Leu	Leu	Gly	Gln	Met	Arg	Arg	Leu	Pro
		35						40				45			

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
 50 55 60  
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
 65 70 75 80  
 His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
 85 90 95  
 Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
 100 105 110  
 Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val  
 115 120 125  
 Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp  
 130 135 140  
 Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu  
 145 150 155 160  
 Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met  
 165 170 175  
 Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser  
 180 185 190

Glu Lys

<210> 12  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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 20 25 30  
 Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
 35 40 45  
 Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu

50		55		60
Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu				
65		70		75
				80
His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser				
	85		90	95
Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu				
	100		105	110
His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly				
	115		120	125
Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys				
	130		135	140
Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser				
145		150		155
				160
Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser				
	165		170	175
Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu				
	180		185	190
Ser Ser Pro				
195				

<210> 13  
 <211> 195  
 <212> PRT  
 <213> Equus caballus

<400> 13
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Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu
20                      25                      30
Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
35                      40                      45
Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
50                      55                      60

Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu  
100 105 110

Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly  
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys  
130 135 140

Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu  
180 185 190

Gly Ser Pro  
195

<210> 14  
<211> 195  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr  
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
195

<210> 15

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus  
sequence

<400> 15

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser  
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln  
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys  
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu  
50 55 60

Gln  
65

<210> 16  
<211> 166  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
1 5 10 15  
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
20 25 30  
Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
35 40 45  
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
50 55 60  
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
65 70 75 80  
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
85 90 95  
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
100 105 110  
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
115 120 125  
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
130 135 140  
Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu  
145 150 155 160  
Thr Gly Tyr Leu Arg Asn  
165

<210> 17  
<211> 165  
<212> PRT  
<213> Homo sapiens

<400> 17

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn  
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
145 150 155 160

Leu Arg Ser Lys Glu  
165

<210> 18

<211> 189

<212> PRT

<213> Mus musculus

<400> 18

Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr  
1 5 10 15

Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu  
20 25 30



Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser  
 35 40 45

Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu  
 50 55 60

Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu  
 65 70 75 80

Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser  
 85 90 95

Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu  
 100 105 110

His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly  
 115 120 125

Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg  
 130 135 140

Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser  
 145 150 155 160

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser  
 165 170 175

Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys  
 180 185

<210> 19  
 <211> 195  
 <212> PRT  
 <213> Antilocapra americana

<400> 19  
 Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr  
 1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro  
 20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser  
 35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu  
 50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu  
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly  
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys  
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser  
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser  
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu  
180 185 190

Ala Ser Ser  
195

<210> 20

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus  
sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala  
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile  
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val  
35 40

<210> 21  
 <211> 184  
 <212> PRT  
 <213> Equus caballus

<400> 21  
 Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys  
           1                  5                  10                  15  
 His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu  
                   20                  25                  30  
 Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser  
           35                  40                  45  
 Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu  
           50                  55                  60  
 Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val  
           65                  70                  75                  80  
 His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser  
                   85                  90                  95  
 Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu  
           100                  105                  110  
 Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly  
           115                  120                  125  
 Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg  
           130                  135                  140  
 Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
           145                  150                  155                  160  
 Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser  
                   165                  170                  175  
 Ser Ser Thr Asn Leu Pro Gln Ser  
           180

<210> 22  
 <211> 92  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus  
sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu  
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys  
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp  
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly  
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala  
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln  
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

gcctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg 60  
tctgaacttg aagacacccc acattccaag atgcccaggg ttcttgggaa tgcttggggg 120  
tcttcgatcc ggaaaatcct accggcatcc tcttagggag ggattattat tattattttt 180  
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc 240  
catggatata actgaataag cggctcaggg ctttccccgc gtggacgtcc gaggccacca 300  
tctgcctgca ttcgccggag ccgccggagg gttagctcg agtctgtctc gggcggggaa 360  
ggatgcgtgg ccgagccggg gagcccgggc gcccgcgga gccggcctcg gtgccacca 420  
gccgggggta gatgctgcct cgcccaggcg ctgagtacc agaccatgga gacctgctt 480  
ggtggcctgc tagcgttttg catggcgttt gccgtggtcg acgcctgcc caagtactgt 540  
gtctgccaga atctgtctga gtcactgggg acctgtgcc cctccaaggg gctgtctttt 600  
gtacccccctg atattgaccg gcggacagtg gagctgcgcc tgggcggcaa cttcatcatc 660  
cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720  
aacaccatca gccacatcca gcccttttcc tttctggacc tcgagagcct ccgtccctg 780  
catcttgaca gcaatcggt gccaaagcctt ggggaggaca ccctccgggg cctgggtcaac 840  
ctgcagcacc ttatcgtgaa caacaaccag ctgggcggca tcgcagatga ggcttttgag 900  
gacttctgac tgacattgga ggatctggac ctctctaca acaacctcca tggcctgccg 960  
tgggactccg tgcgacgcat ggtcaacctc caccagctga gcctggacca caacctgctg 1020

gatcacatcg ccgagggcac ctttgcagac ctgcagaaac tggcccgccct ggatctcacc 1080  
tccaatcggc tgcagaagct gcccctgat cccatctttg cccgctccca ggcttcggct 1140  
ttgacagcca caccctttgc cccacccttg tcccttagtt ttgggggtaa cccacttcac 1200  
tgcaattgtg agcttctctg gctgcgagg ctgagcgagg acgatgacct ggaaacctgt 1260  
ggctccccag ggggcctcaa gggtcgctac ttctggcatg tgcgtgagga ggagtttgtg 1320  
tgcgagccgc ctctcatcac ccagcacaca cacaagttgc tggttctgga gggccaggcg 1380  
gccacactca agtgcaaagc cattggggac cccagccccc ttatccactg ggtagccccc 1440  
gatgaccgcc tggtagggaa ctctcaagg accgctgtct atgacaatgg caccctggac 1500  
atcttcatca ccacatctca ggacagtggg gccttcacct gcattgctgc caatgctgcc 1560  
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accagccgca ctgcaccccc caagtccgc ctctcagaca tctactggctc cagcaagacc 1680  
agccggggag gtggaggcag tgggggcgga gagcctccca aaagccccc ggaacgggct 1740  
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tacaggatga tcccagcctc caacaaggcc ttctgtgtca acaacctggg gtcagggact 1920  
ggctacgact tgttgtgtgt ggccatgtgg gatgacacag ccacgacact caccggccacc 1980  
aacatcgtgg gctgcgcccc gttcttcacc aaggctgact acccgagtg ccagtccatg 2040  
cacagccaga ttctggggcg caccatgatc ctggctcatc ggggcatcat cgtggccacg 2100  
ctgctgggtc tcatcgtcat cctcatggg cgctacaagg tctgcaacca cgaggccccc 2160  
agcaagatgg cagcggccgt gagcaatgtg tactcgaga ccaacggcgc ccagccaccg 2220  
cctccaagca gcgcaccagc cggggccccc cgccagggcc cgccgaagg ggtgggtgcg 2280  
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gccccgcgcc ccaagcccag ccttgaccgc ctgatggggg ccttcgcctc cctggacctc 2460  
aagagtcaga gaaaggagga gctgctggac tccaggactc cagccgggag aggggctggg 2520  
acgtcggccc ggggcccacca ctcgaccga gagccactgc tggggccccc tgcggcccg 2580  
gccaggagcc tgctcccctt gccgttgag ggcaaggcca aacgcagcca ctccctcgac 2640  
atgggggact ttgctgctgc ggcggcggga ggggtcgtgc cgggcggcta cagtccctc 2700  
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gagagcacgg tctaggtggg ggtgggcatg ctccctttcc tgtgcgcagg gtgggagaag 2880  
gggaaagaat ctactggca agtgtttgtg gagtttccat ggtgatgttt acatccaggg 2940  
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cctccccacc acccgccgg ggtgtgctca gggaatgtgg actcgctcaa atgccggact 3060  
gagccctgag tgtttggaag ggcgagactc cgctttcta atcacaatg tagcctacaa 3120  
gcaagcggct ttggattgct tatg 3144

<210> 24  
<211> 832  
<212> PRT  
<213> Homo sapiens

<400> 24  
Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser  
1 5 10 15  
Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg

	20		25		30
Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu					
	35		40		45
Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys					
	50		55		60
Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu					
	65		70		75
Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg					
		85		90	95
Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg					
	100		105		110
Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg					
	115		120		125
Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser					
	130		135		140
Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu					
	145		150		155
Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn					
	165		170		175
Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu					
	180		185		190
Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro					
	195		200		205
Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp					
	210		215		220
His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln					
	225		230		235
Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro					
	245		250		255
Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr					
	260		265		270
Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His					

275		280		285
Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp				
290		295		300
Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp				
305		310		315
				320
His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln				
		325		330
				335
His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys				
		340		345
				350
Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro				
		355		360
				365
Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn				
		370		375
				380
Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe				
385		390		395
				400
Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu				
		405		410
				415
Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr				
		420		425
				430
Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr				
		435		440
				445
Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro				
450		455		460
Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu				
465		470		475
				480
Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln				
		485		490
				495
Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile				
		500		505
				510
Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr				
		515		520
				525
Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr				

530		535		540
Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala				
545		550		555 560
Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr				
	565		570	575
Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe				
	580		585	590
Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro				
	595		600	605
Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly				
	610		615	620
Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln				
	625		630	635 640
Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala				
	645		650	655
Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser				
	660		665	670
Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser				
	675		680	685
Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala				
	690		695	700
Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg				
	705		710	715 720
Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser				
	725		730	735
Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu				
	740		745	750
Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp				
	755		760	765
Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly				
	770		775	780
Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu				



785		790		795		800
Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly						
	805		810		815	
Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val						
	820		825		830	

<210> 25  
 <211> 98  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:IFAbd Domain  
 13-110

<400> 25
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
1 5 10 15
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
20 25 30
Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
35 40 45
His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
50 55 60
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
65 70 75 80
Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
85 90 95
Ile Val

<210> 26  
 <211> 183  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143

Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys  
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg  
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys  
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly  
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn  
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala  
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln  
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu  
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg  
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr  
165 170 175

Tyr Ser Ser Thr Ala Leu Gln  
180